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Numerical Taxonomic analysis for the estimation of Genetic Diversity among some traditional rice (*Oryza sativa* L.) varieties of West Bengal

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Abstract: The use of numerical taxonomy in plant systematics is crucial because it allows for the improvement of traditional taxonomic data gathered from sources like as morphology, physiology, chemistry, anatomy, and cytology, among others, by utilizing a better and greater number of documented features. It has been determined that it is crucial to keep track of crop genetic resource management dynamics using the fundamental diversity data of traditional crop varieties or landraces. The protection of rice diversity and the use of diversity for rice breeding are strongly tied to the food security of this region because rice is the most significant staple food in South-East Asia. Traditional rice types continue to grow in many indigenous societies despite the relentless advance of modernization, which includes industrialization and land use rules focused on the market. Folk rice varieties are also grown in various areas of West Bengal. The genetic diversity among these traditional or folk types is the only source for future rice enhancement. In this study, many local rice varieties were gathered from various regions of West Bengal, and "richness data" was calculated utilizing this knowledge. Additional data on agro-morphological traits revealed considerable variations between genotypes. Wide variance among the folk rice genotypes was revealed by estimating mean, range, standard deviation, standard error, and coefficient of variation. Following numerical taxonomic analysis, classification of genotypes revealed high genetic diversity among West Bengal's traditional rice varieties. This genetic variety might be utilised in rice breeding, where it is challenging to get access to new technology.

Introduction

Oryza sativa L., a cereal crop important for food security, is a staple in the diets of many billions of people worldwide. Over one third of the world's population depends on it as their main source of sustenance. The world's demand for food production, particularly rice, is expected to rise in the future decades as a result of the population growth (Das et al., 2013; Mbe et al., 2022). The use of different mathematical operations on character state data that has been numerically encoded is known as numerical taxonomy or phenetics. Sokal and (1963) Sneath created the early design of the idea, which they later developed further. In numerical taxonomy, numbers and codes are assigned to all the characters and every character is given equal importance. Numerical taxonomy can improve other domains such as morphology, physiology, chemistry, anatomy, and cytology since it uses more recorded features than traditional taxonomic data from sources like these. Numerical taxonomy is of major importance in plant systematics (James et al., 2020; De and Dey, 2019). It is common practice to research genetic diversity using morphological descriptors and molecular markers in order to design conservation strategies and facilitate their management (Sharma et al., 2021)

Genetic diversity analysis of crop plants

Crop improvement benefits from knowledge of genetic interactions between various genotypes and genetic diversity. The selection of various parental combinations, accurate classification of accessions, and precise variety identification all benefit from genetic diversity analysis. It has been determined that it is crucial to track crop genetic resource management dynamics to have access to fundamental diversity data of traditional varieties or landraces. In South-East Asia, rice is the most significant staple food. The conservation of rice diversity and the use of that diversity for rice breeding directly impact the food security of this region. Before implementing an effective and worthwhile breeding strategy, it is essential to understand the genetic variety in the gene pool (Lapitan et al., 2007; Emi et al., 2021). It has been found that using different parents in hybridization programs results in better hybrids (Subramanian and Subbaraman, 2010). Having a diverse genetic population protects against crop failure (Subba Rao et al., 2001). Farmers, researchers, decision-makers, and environmentalists have expressed grave alarm recently about the ongoing loss of the genetic variety of rice cultivars (Singh et al., 2000). The twentieth century's major breeding initiatives played a significant role in the decline of crop genetic diversity (Gepts, 2006). The loss of diversity within species within the same population is of concern, not the extinction of a particular species like wheat or rice.

The proportion of genetic diversity present at various levels is a key factor in breeding program success. It has been discovered that basic diversity information on folk varieties or landraces is crucial for tracking crop genetic resource management dynamics. The number of such folk variants or landraces in the community is counted to calculate the landrace or folk variety's "richness," which is a quick and accurate method for estimating diversity. Folk varieties or landraces have a vast amount of the most desirable genes, which can be efficiently used in modern breeding programs to create rice varieties that are not only superior in quality and production potential but also resilient to biotic and abiotic challenges (Saxena et al., 1988).

The preservation of rice landraces is now viewed as a need rather than a luxury (Chang, 1984). Because of the cultural values embodied in landraces, this crop's genetic variety may be preserved (Deb and Malhotra, 2001). In West Bengal, rice is grown in a variety of traditional folk varieties and used in several customs and rituals (De, 2010; De, 2019). The only resource accessible for rice enhancement in the future is the genetic diversity among various traditional rice types. Genetic diversity solely refers to varietal variation in terms of farming, which farmers can distinguish based on agro morphological qualities, phenological characteristics, postharvest traits, and differential adaptation performance under abiotic and biotic pressures (De et al., 2010; De and Dey, 2022).

Many indigenous tribes still practice landraces despite modernisation's relentless advance, including industrialization and market-driven land usage rules (Deb and Malhotra, 2001). The greatest way to ensure that the impoverished have "acceptable livelihoods" is by incorporating traditional rice cultivars and cultural norms into locally based and regulated farming systems (Cleveland et al., 1994). Several supply and demand considerations influence any crop's decision to grow a modern variety against a landrace. For on-farm conservation, landraces must have specific characteristics that the farmer deems important (De et al., 2011; De and Dey, 2021).

The main objective of this study was to study genetic diversity in some of the still extant landraces of West Bengal and selected cultivars of rice using agro-morphological, grain morphological and grain/kernel dimension data. Principles of Numerical Taxonomy of Sneath and Sokal (1973) were used to infer the results. This information on the existing genetic diversity will be useful for selecting parents for future rice breeding programs.

Materials and Methods
Plant material

Twenty rice varieties were used in this investigation. The rice genotypes used were adapted to varied climatic and edaphic conditions of West Bengal. These accessions were collected from different agro-climatic belts of West Bengal, and studied under field conditions for two consecutive years. There were 13 (Thirteen) non aromatic folk varieties/ landraces of West Bengal (NA WBL) and 3 (three) aromatic folk varieties/ landraces of West Bengal (A WBL). Checks included 4 (Four) indigenous (of Indian origin) high-yielding cultivars (HYV) obtained from CRRS (Chinsura Rice Research Station). The details of the rice genotypes used in this study are given in Table 1.

Experimental design

Three replicates of 40 plants each were used in the randomized block design (RBD) to grow the different rice genotypes. On the last week of June, seeds were sowed in the seed bed, and after 30 days, one robust seedling or hill was transplanted at a row x plant spacing of 25cm x 15cm. The usual agronomic procedures were

used. At 85% of the seeds' maturity, harvesting was completed.

different characters were estimated following the procedure described by Singh and Narayanan (1993).

Table 1. The rice genotypes used in this study: genotype name, place of adaptation/source and type of cultivar.

Sl. No	Genotypes	Context for adaptation/source	Origin	Type of cultivar
1	Kajaldekhi	Cooch Behar	CL, SF	NA WBL
2	Chottonunia	Cooch Behar	CL SF	NA WBL
3	Bochi	Cooch Behar	CL, SF	NA WBL
4	Jashoa	Cooch Behar	CL, SF	NA WBL
5	Fulpankhari	Cooch Behar	CL, SF	NA WBL
6	Pankhari	Cooch Behar	CL, SF	NA WBL
7	Malshira	Cooch Behar	CL SF	NA WBL
8	Kalonunia	Cooch Behar	CL, SF	A WBL
9	Khejurchari	24 PGS (South)	CL, SF	NA WBL
10	Valki	Coastal Midnapur	CL, SF	NA WBL
11	Mugi	Coastal Midnapur	CL, SF	NA WBL
12	Champakushi	Coastal Midnapur	CL SF	NA WBL
13	Dudhsar	Coastal Midnapur	CL, SF	NA WBL
14	Kankri	Coastal Midnapur	CL, SF	NA WBL
15	Sabita	CRRS, WB, INDIA	CD from several crosses	HYV INA
16	Kumargore	CRRS, WB, India	CD from several crosses	HYV INA
17	Meghi	CRRS, WB, India	CD from several crosses	HYV INA
18	Matla	CRRS, WB, India	CD from several crosses	HYV INA
19	Radhunipagol	Chakdah, Nadia	CL SF	A WBL
20	Kataribhog	Chakdah, Nadia	CL, SF	A WBL

A WBL = Aromatic West Bengal landrace, **CD** = Complex derivative, **CL** = Collection line**, CRRS**= Chinsura Rice Research Station, **HYV** = High yielding, **NA** = Non-aromatic, **INA** = Indigenous non-aromatic, **NA WBL** = Non aromatic West Bengal landrace, **SF** = Slf-fertilized.

Assessment of genetic diversity

A total of 10 traits were measured at various growth stages. Characterization was carried out in accordance with the International Rice Research Institute's (IRRI) Standard Evaluation System (SES) for rice (IRRI, 2002). The trait characterization was divided into the following groups viz. agronomic and morphological traits. All these trait characterization were actual measurements or counts. A total of five plants per replication per rice line were sampled at random, avoiding the border rows for characterization. Minimum 3 replications were taken.

The list of 10 characters in an alphabetical manner is viz., Best Panicle Length (BPL), Best Panicle weight (BPW), Days to Flowering (DTF), Days to Maturity (DM), Flag Leaf Length (FLLNTH), 100 (Hundred) Seed Weight (100SW), Number of Panicles per Plant (PANNO), Plant Height (PLHT), Total Panicle Weight (TPW) and Total Straw Weight (TSW). Mean, range, standard error of mean and standard deviation for

Results and Discussion

For a species to survive and adapt to changing circumstances, there must be a certain level of genetic diversity within that species (Gao, 2003). The characterisation revealed a tremendous degree of variety even though the majority of the rice genotypes belonged to *Oryza sativa* L. The ability of the native farmers to create and maintain a variety of landraces is reflected in this variance. Dwindling genetic wealth erodes the capacity to maintain and enhance agricultural productivity. Table 2 shows the estimation of the mean, range (minimum value – maximum value), standard deviation (SD) and standard error of the mean (SE) for different plant characters. This table indicated wide genetic diversity among genotypes for all the characters studied. A very wide range was observed in the total straw weight (TSW). There was sufficient variation in the days to maturity (DM) and plant height (PLHT). The graphical representation of some of the important quantitative agro-morphological traits is shown in figure

1. There is considerable variation in the panicle number (PANNO), flag leaf length (FLLNTH) and total panicle weight (TPW) among the folk rice varieties.

The length of the flag leaf is an important parameter that directly affects the total yield as it is directly proportional to the photosynthetic rate.

Table 2. Genetic parameters of variation for the quantitative traits among the rice genotypes.

| Sl. No	Characters	Mean	Range		Standard deviation	SE of mean
			Minimum	Maximum		
1	Plant Height (PLHT) in cm	163.433	119	193	13.0959	0.1874
2	Flag Leaf Length (FLLNTH) in cm	36.53	22	66	6.78349483	0.1253
3	Number of Panicles per Plant (PANNO).	7.433333333	3	16	2.572924638	0.054
4	Best Panicle Length (BPL) in cm	26.2233	18	34	2.88751	0.032
5	Best Panicle weight (BPW) in grams.	2.758	0.8	6.5	1.221239	0.042
6	100 (Hundred) Seed Weight (100SW) in grams.	2.255	1	3.4	0.60404687	0.023
7	Total Panicle Weight in grams (TPW).	13.14533	3.1	37.26	5.22936	0.083
8	Total Straw Weight (TSW) in grams.	32.01	5	74	12.181	0.12
9	Days to Flowering (DTF) in days.	95.8	85	112	7.54093674	0.044
10	Days to Maturity (DM) in days.	140.15	111	160	15.49027069	0.075
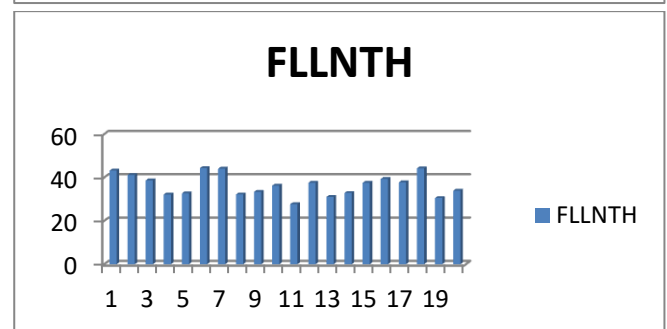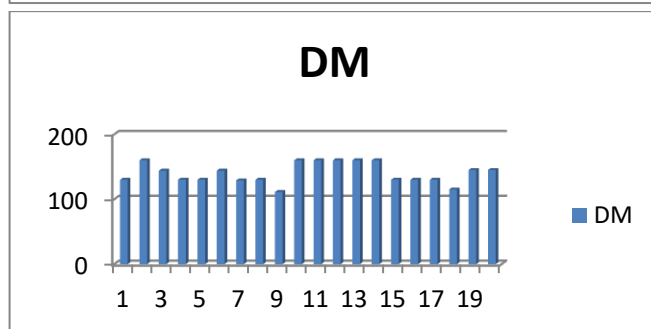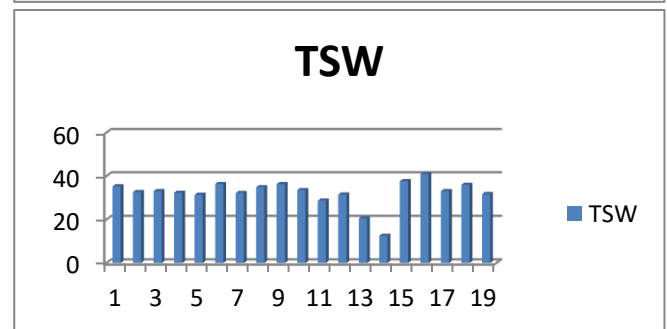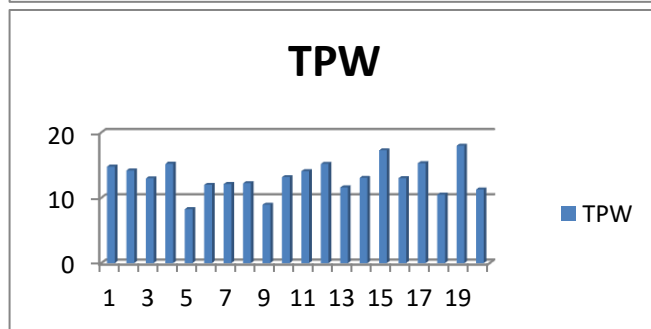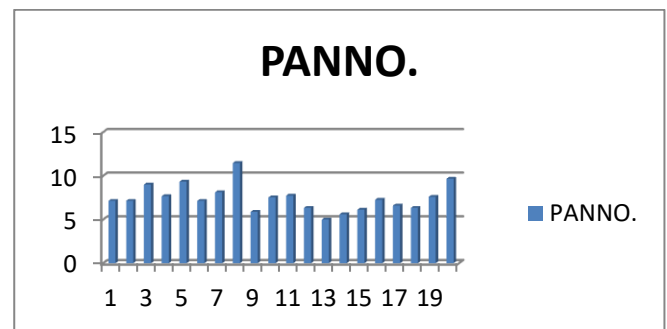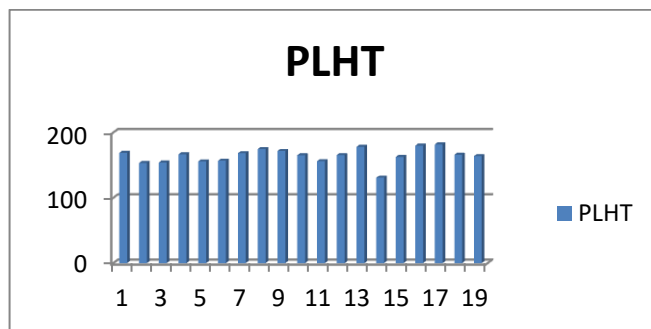
Figure 1. Graphical representation of the variation of some important agro-morphological quantitative traits among the 20 rice varieties
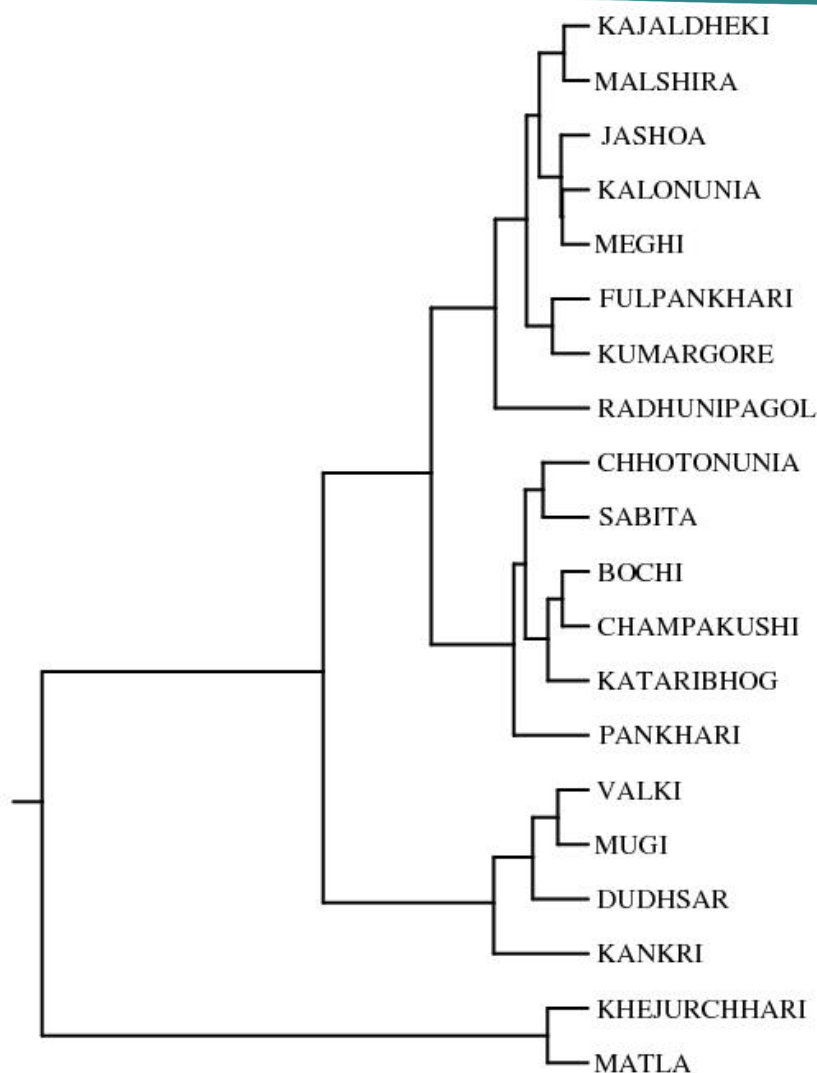
Figure 2. Dendrogram based on the agro-morphological characters.

The genotypes' plant heights ranged from 119 cm to 193 cm, while the average number of panicles per plant was 7.43, with panicles ranging from 3 to 16. The best panicle length, total panicle weight, total straw weight, days to flowering, and days to maturity all showed similar variations.

The level of uncontrolled variation present in the sample is shown by the standard error of the mean in relation to several features. The trustworthiness of estimations in various situations was shown by the standard error of the mean, which was highest (0.1874) for plant height and lowest (0.12%) for total straw weight. This outcome is consistent with those of Singh et al. (2010).

Cluster analysis based on morphology suggested that the accessions could be grouped. Genotypes were classified into 4 (four) clusters following the numerical taxonomic analysis of Sneath and Sokal (1963). For any plant improvement endeavour such cluster analysis may be helpful in the selection of the parents in the plant breeding project.

Conclusion

Numerical taxonomic analysis has helped in estimating the genetic diversity among the traditional rice varieties in this investigation. It is imperative to choose the parents for the cross to develop new varieties very carefully. Once lost, they are lost forever. Studies on the genetic diversity analysis among rice germplasm have increased in recent years (Singh et al., 2000; Singh et al., 2010; Parikh et al., 2012). This study reveals that the 'richness' of the folk rice varieties of West Bengal is quite high. Despite the rampant cultivation of high yielding varieties (HYVs) several folk varieties are still cultivated in pockets of West Bengal especially on the marginal land where the high yielding varieties (HYVs) do not perform well. Plant genetic resources are among the most vulnerable of all non-renewable natural resources. This investigation is part of a long-term project aimed at collecting, identifying and documenting the folk rice variety diversity of West Bengal. With the recent emphasis on the documentation of the traditional knowledge (TK) of plant genetic resources, this study will contribute to the documentation of the genetic

diversity of the rich folk rice genetic wealth of West Bengal.

References

Chang, T. T. (1984). Conservation of rice Genetic Resources: Luxury or Necessity? *Science*, *224*, 251-256. https://doi.org/10.1126/science.224.4646.251

Cleveland, D. A., Soleri, D., & Smith, S. E. (1994). Do folk crop varieties have a role in sustainable agriculture? *Bioscience*, *44*, 740-751. https://doi.org/10.2307/1312583

Das, B., Sengupta, S., Parida, S.K., Roy, B., Ghosh, Prasad, M., & Ghose, T.K. (2013). Genetic diversity and population structure of rice landraces from Eastern and North Eastern States of India. *BMC Genetics*, *14*, 71. https://doi.org/10.1186/1471-2156-14-71

Deb, D., & Malhotra, K. C. (2001). Conservation Ethos in Local Traditions: The West Bengal Heritage. *Society and Natural Resources*, *14*, 711–724. https://doi.org/10.1080/08941920152524909

De, M., Bandyopadhyay, S., Dey, S. R., Das, B., Sengupta, S., & Ghose T. K. (2011). On-Farm Conservation of Rice Landrace Genetic Diversity In West Bengal. Emerging Trends in Plant Science (ISBN- 978-93-80673-52-3) Edition 1, Proceedings of UGC Sponsored National Level Seminar Organized by PG Department of Botany, Barasat Government College in Collaboration with Indian Statistical Institute, Kolkata on 14th & 15th July, 2011 pp. 37-45.

De, M. (2010). Folk rice varieties and Folklore. Proceedings of the UGC sponsored seminar, Multiverse of Folk cultures; An Eastern Perspective, in collaboration with Sahitya Akademi, 5-6 February, 2010, pp. 46-57.

De, M. (2019). Documentation of the grain morphological variation within some traditional aromatic rice (*Oryza sativa* L.) varieties of West Bengal. *International Journal of Experimental Research and Review*, *18*, 22-26. https://doi.org/10.52756/ijerr.2019.v18.004

De, M., Bandyopadhyay, S., Dey, S. R., Das, B., Sengupta, S., Debnath, M., & Ghose T. K. (2010). Evaluation of Genetic Diversity in Rice (*Oryza sativa* L.) Landraces of West Bengal by Agromorphological Characterisation. Proceedings of the State Level Seminar on 'Playing God: expanding Frontiers of Biotechnology' 6th and 7th November, 2009, organized by Gurudas College, Kolkata in collaboration with Indian Institute of Chemical Biology, Kolkata, West Bengal, India, pp. 65-69.

De, M., & Dey, S. R. (2019). An overview on Taxonomic Keys and Automated Species Identification (ASI). *International Journal of Experimental Research and Review*, *20*, 40-47. https://doi.org/10.52756/ijerr.2019.v20.004

De, M., & Dey, S. R. (2021). Variation in agronomic characters among traditional rice varieties of Cooch Behar, West Bengal: A Case Study. *International Journal of Experimental Research and Review*, *25*, 1-8. https://doi.org/10.52756/ijerr.2021.v25.001a

De, M., & Dey, S. R. (2022). Variation in the stored grain pest *Sitotroga cerealella* (Olivier) infestation at low and high moisture storage conditions among some indigenous rice genotypes of West Bengal. *International Journal of Experimental Research and Review*, *28*, 47-54. https://doi.org/10.52756/ijerr.2022.v28.007

Emi, F. R., Khatun, H., Yasmine, F., Hasan, A. K., & Hossain, M. A. (2021). Morphological variability and genetic diversity of Aman rice germplasm of Bangladesh cultivated in Mymensingh region. *Plant Science Today*, *8*(4), 972–985. https://doi.org/10.14719/pst.1304

Gao, L. (2003). The conservation of Chinese rice biodiversity: genetic erosion, ethnobotany and prospects. *Genetic Resources and Crop Evolution*, *50*, 17–32. https://doi.org/10.1023/A:1022933230689

Gepts, P. (2006). Plant genetic resources conservation and utilization: the accomplishments and future of a societal insurance policy. *Crop Sci.*, *46*, 2278–2292. https://doi.org/10.2135/cropsci2006.03.0169gas

IRRI. (2002). Standard Evaluation System for Rice (SES). International Rice Research Institute, Los Baños, Philippines.

James, O.E., Green, B. O., Ajuru, M. G., & Wilson, V. (2020). Macro-morphological study on seven selected species of Euphorbiaceae in the Niger

Delta Region of Nigeria. International *Journal of Advanced Academic Research, Sciences, Technology and Engineering*, 6(4), 27- 40.

Lapitan, V. C., Brar, D. S., Abe, T., & Redona, E. D. 2007. Assessment of genetic diversity of Philippine rice cultivars carrying good quality traits using SSR markers. *Breeding Science*, *57*, 263-270. https://doi.org/10.1270/jsbbs.57.263

Mbe, J. O., Saraswathi, R., Jeyaprakash, P., & Awah, J.I. (2019). Evaluation of genetic diversity for quantitative traits in rice (*Oryza sativa* L.) genotypes. *Nigerian Agricultural Journal*, *50*(1), 200-207

Parikh, M., Motiramani, N. K., Rastogi, N. K., & Sharma, B. (2012). Agro-morphological characterization and assessment of variability in aromatic rice germplasm. *Bangladesh J. Agril. Res*., *37*(1), 1-8. https://doi.org/10.3329/bjar.v37i1.11168

Saxena, R.K., Chang, T. T., Sapra, R.L., & Paroda, R.S. (1988). Evaluation studies in indigenous rice (*Oryza sativa* L.) germaplasm at IRR1. Philippines. Published in NBPGR manual. pp. 1-3.

Sharma, M., Abdullah, G.M., Salgotra, R.K., Hangloo, S., Punya, Singh, A.K., Sharma, V., & Amarinder Singh, A. (2021). Genetic diversity analysis in rice (*Oryza sativa* L.) germplasm of Jammu region of Jammu and Kashmir. *Indian J.* *Genet*., *81*(4): 529-537. doi: 10.31742/ISGPB.81.4.5

Singh, P., & Narayanan, S.S. (1993). Biometrical techniques in plant breeding. Kalyani Publishers, New Delhi, pp. 83.

Singh, R. K., Singh, U.S., & Khush, G.S. (2000). Aromatic Rices. New Delhi: Oxford and IBH Publishing Company. Pvt Limited.

Singh, B., Mishra, M. K., & Naik, R. K. (2010). Genetic diversity among some traditional Aromatic Rice (*Oryza sativa* L.) varieties of Orissa. *Indian J. Agric. Res*., *44*(2), 141–145.

Sokal, R.R., & Sneath, P.H.A. (1963). Principles of Numerical Taxonomy. W.H. Freeman & Co., New York.

Sneath, P.H.A., & Sokal, R.R. (1973). Principles of numerical taxonomy (7 Ed.). San Francisco: W.H. Freeman. ISBN, 0-7167-0621-0.

Subba Rao L.V., Prasad, G.S.V., Prasada Rao, U., Rama Prasad, A., Acharyulu, T.L., & Rama Krishna, S. (2001). Collection, characterization and evaluation of rice germplasm from Bastar Region. *Indian J. Plant. Genet Resour*., *14*, 222-224

Subramanian, A., & Subbaraman, N. (2010). Hierarchical cluster analysis of genetic diversity in Maize germplasm. *Electronic Journal of Plant Breeding*, *1*(4), 431-436.